Pathogenicity in *Heterobasidion annosum*

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Heterobasidion annosum is one of the major pathogens to conifers in the Northern Hemisphere. Research has been carried out to characterise the molecular mechanism of the pathogenicity in this basidiomycete. One factor that has limited the research about *H. annosum* pathogenesis is the lack of coding sequence information. Therefore, a project on producing sequence data from *H. annosum* by generating ESTs has been carried out. The collection of sequence data will assist future research on *H. annosum* together with the high density cDNA arrays that were also constructed in this work. It is interesting that 30% of the genes identified did not have any similarity to any known proteins and 16% had similarity only with proteins with unknown functions. Recently, progress has been made in work on mapping the pathogenicity factors in *Heterobasidion* using a hybrid between North American P and S homokaryons. Based on AFLP markers, a genetic linkage map was established that allowed for mapping QTLs for pathogenic growth towards seedling roots and pine innerbark. The next step underway is to verify the identity of candidate genes located within the established region of the genome. Future functional analysis of both QTL and EST-derived candidate genes should be aided by the recently established *Agrobacterium*-mediated transformation system in *Heterobasidion*.

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